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RAW SEQUENCE LISTING   DATE: 02/06/2002
PATENT APPLICATION: US/10/054,295   TIME: 15:49:16

Input Set : N:\Crf3\RULE60\10054295.raw
Output Set: N:\CRF3\02062002\J054295.raw

SEQUENCE LISTING

```
  3  (1) GENERAL INFORMATION:
  5        (i) APPLICANT: Cech, Thomas R.
  6                       Lingner, Joachim
  7                       Nakamura, Toru
  8                       Chapman, Karen B.
  9                       Morin, Gregg B.
 10                       Harley, Calvin
 11                       Andrews, William H.
 13       (ii) TITLE OF INVENTION: Novel Telomerase
 15      (iii) NUMBER OF SEQUENCES: 225
 17       (iv) CORRESPONDENCE ADDRESS:
 18            (A) ADDRESSEE: Townsend and Townsend and Crew LLP
 19            (B) STREET: Two Embarcadero Center, 8th Floor
 20            (C) CITY: San Francisco
 21            (D) STATE: California
 22            (E) COUNTRY: United States of America
 23            (F) ZIP: 94111
 25        (v) COMPUTER READABLE FORM:
 26            (A) MEDIUM TYPE: Floppy disk
 27            (B) COMPUTER: IBM PC compatible
 28            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 29            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 31       (vi) CURRENT APPLICATION DATA:
 32            (A) APPLICATION NUMBER: US/10/054,295
 33            (B) FILING DATE: 18-Jan-2002
 54            (C) CLASSIFICATION: 536
 51      (vii) PRIOR APPLICATION DATA:
 37            (A) APPLICATION NUMBER: 08/854,050
 38            (B) FILING DATE:
 42            (A) APPLICATION NUMBER: US 08/846,017
 43            (B) FILING DATE: 25-APR-1997
 47            (A) APPLICATION NUMBER: US 08/844,419
 48            (B) FILING DATE: 18-APR-1997
 52            (A) APPLICATION NUMBER: US 08/724,643
 53            (B) FILING DATE: 01-OCT-1996
 56     (viii) ATTORNEY/AGENT INFORMATION:
 57            (A) NAME: Apple, Randolph T.
 58            (B) REGISTRATION NUMBER: 36,429
 59            (C) REFERENCE/DOCKET NUMBER: 015389-002930US
 61       (ix) TELECOMMUNICATION INFORMATION:
 62            (A) TELEPHONE: (415) 576-0200
 63            (B) TELEFAX: (415) 576-0300
```

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C--> 32
C--> 33

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65 (2) INFORMATION FOR SEQ ID NO: 1:
67      (i) SEQUENCE CHARACTERISTICS:
68          (A) LENGTH: 3279 base pairs
69          (B) TYPE: nucleic acid
70          (C) STRANDEDNESS: single
71          (D) TOPOLOGY: linear
73      (ii) MOLECULE TYPE: other nucleic acid
74          (A) DESCRIPTION: /desc = "DNA"
76      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
78  AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA    60
80  TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA   120
82  TCAAGCTGAT AATCATGGCA TTCACTCAGC TCTTAAGACT TGTGAAGAAA TTAAAGAAGC   180
84  TAAAACGTTG TACTCTTGGA TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA   240
86  TTATAAAGAT TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG   300
88  AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT CAACTGGACT   360
90  AATGATCGAA CTTATTGACA AATGCTTAGT TGAACTTCTT TCATCAAGCG ATGTTTCAGA   420
92  TAGACAAAAA CTTCAATGAT TTGGATTTCA ACTTAAGGGA AATCAATTAG CAAAGACCCA   480
94  TTTATTAACA GCTCTTTCAA CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT   540
96  TAGAGCAATG ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA   600
98  GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG ATCATTTGAA   660
100 AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG   720
102 ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGAGAAA GATCACTTTC TCAACAACAT   780
104 CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTATT GCACTCATTT     840
106 TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC   900
108 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTAATA GAATTAGAAA     960
110 GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAG TCAAAGATTT  1020
112 TAACTTCAAC TACTATTTAA CAAAATCTTG TCCTCTTCCA GAAAATTGGC GGGAACGGAA  1080
114 ACAAAAAATC GAAAACTTGA TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA  1140
116 GCTGTTTAGC TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA  1200
118 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC AAAAGAAAGT  1260
120 TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC AAAAACTTAT TGCTTGAGAA  1320
122 GATCAATACA AGAGAAATAT CATGGATGCA GGTTGAGACC TCTGCAAAGC ATTTTTATTA  1380
124 TTTTGATCAC GAAAACATCT ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT  1440
126 CGTCGTCTCG CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA  1500
128 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA TCGCAGACTT  1560
130 AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAGAATGGA AAAAGTCGCT  1620
132 TGGATTTGCA CCTGGAAAAC TCAGACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT  1680
134 GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC  1740
136 GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC  1800
138 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG AGTTTGTTTG  1860
140 CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA ACTATGGATA TCGAAAAGTG  1920
142 ATATGATAGT GTAAACAGAG AAAAACTATC AACATTCCTA AAAACTACTA AATTACTTTC  1980
144 TTCAGATTTC TGGATTATGA CTGCACAAAT TCTAAAGAGA AGAATAACA TAGTTATCGA    2040
146 TTCGAAAAAC TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT  2100
148 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG AACAAAATGA  2160
150 CTTAAATGCA AAGAAACAT TAATTGTTGA AGCAAAGCAA AGAAATTATT TTAAGAAAGA   2220
152 TAACTTACTT CAACCAGTCA TTAATATTTG CCAATATAAT TACATTAACT TTAATGGGAA  2280
154 GTTTTATAAA CAAACAAAAG GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTCATC  2340
156 ATTTTATTAT GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA  2400
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158 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC TTTTGATTAC   2460
160 AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT ATAAACGTAA GTCGTGAAAA   2520
162 TGGATTTAAA TTCAATATGA AGAAACTACA GACTAGTTTT CCATTAAGTC CAAGCAAATT   2580
164 TGCAAAATAC GGAATGGATA GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG   2640
166 GATTGGCATC TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT   2700
168 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT CAATGTGGCT   2760
170 CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC CATTATTTTA GAAAGACGAT   2820
172 TACAACCGAA GACTTTGCGA ATAAAACTCT CAACAAGTTA TTTATATCAG GCGGTTACAA   2880
174 ATACATGCAA TGAGCCAAAG AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG   2940
176 TATGATCGAC TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA   3000
178 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG ACTTTTTCCT   3060
180 TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA AAGTACATTT TCAACAGAGT   3120
182 TTGCATGATC CTCAAGGCAA AAGAAGCAAA GCTAAAAAGT GACCAATGTC AATCTCTAAT   3180
184 TCAATATGAT GCATAGTCGA CTATTCTAAC TTATTTTGGA AAGTTAATTT TCAATTTTTG   3240
186 TCTTATATAC TGGGGTTTTG GGGTTTTGGG GTTTTGGGG                          3279
188 (2) INFORMATION FOR SEQ ID NO: 2:
190       (i) SEQUENCE CHARACTERISTICS:
191            (A) LENGTH: 1031 amino acids
192            (B) TYPE: amino acid
193            (C) STRANDEDNESS: Not Relevant
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W--> 194   (D) TOPOLOGY: **Not Relevant**
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196       (ii) MOLECULE TYPE: protein
198       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
200       Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
201       1               5                   10                  15
203       Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
204                   20                  25                  30
206       Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
207               35                  40                  45
209       Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
210           50                  55                  60
212       Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
213       65                  70                  75                  80
215       Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
216                   85                  90                  95
218       Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln
219                   100                 105                 110
221       Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu
222                   115                 120                 125
224       Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp
225           130                 135                 140
227       Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr
228       145                 150                 155                 160
230       Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln
231                   165                 170                 175
233       Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
234                   180                 185                 190
236       Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
237                   195                 200                 205
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239    Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu
240        210             215              220
242    Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg
243    225             230              235                  240
245    Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys
246                245              250                  255
248    His Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala
249                260              265                  270
251    Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys
252            275              280                  285
254    Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val
255        290              295              300
257    Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro
258    305             310              315                  320
260    Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys
261                325              330                  335
263    Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr
264                340              345                  350
266    Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn
267                355              360                  365
269    Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln
270        370              375                  380
272    Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His
273    385                 390                  395                  400
275    Lys Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met
276                405              410                  415
278    Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn
279                420              425                  430
281    Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val
282            435              440                  445
284    Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser
285        450              455              460
287    Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met
288    465             470              475                  480
290    Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln
291                485              490                  495
293    Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly
294                500              505                  510
296    Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr
297            515              520                  525
299    Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr
300        530              535              540
302    Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys
303    545             550              555                  560
305    Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp
306                565              570                  575
308    Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val
309                580              585                  590
311    Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
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312           595              600              605
314    Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
315        610              615              620
317    Leu Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg
318    625              630              635                  640
320    Lys Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met
321                645              650              655
323    Lys Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly
324            660              665              670
326    Gln Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu
327            675              680              685
329    Asn Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe
330        690              695              700
332    Lys Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn
333    705              710              715                  720
335    Tyr Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro
336                725              730                  735
338    Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr
339                740              745              750
341    Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro
342            755              760              765
344    Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu
345        770              775              780
347    Leu Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu
348    785              790              795                  800
350    Ile Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu
351                805              810              815
353    Gln Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met
354                820              825              830
356    Asp Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile
357            835              840              845
359    Gly Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn
360        850              855              860
362    Leu Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr
363    865              870              875                  880
365    Lys Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met
366                885              890              895
368    Asn Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe
369            900              905              910
371    Ala Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr
372        915              920              925
374    Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala
375        930              935              940
377    Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val
378    945              950              955                  960
380    Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile
381                965              970                  975
383    Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His
384            980              985              990
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Input Set : **N:\Crf3\RULE60\10054295.raw**
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L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:194 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=2
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L:3506 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 68
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L:7766 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216
L:7791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7794 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7797 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7908 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
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